

```

1 MRENMARGPCNAPRWVSLMVLVAIGTAVTA AVNPGVVVRISQKGLDYASQ 50
  |||||
1 MRENMARGPCNAPRWVSLMVLVAIGTAVTA AVNPGVVVRISQKGLDYASQ 50
  |||||
51 QGTAALQKELKRIKIPDYSDFEIKHLKGCHYFYSMDIREFQLPSSQIS 100
  |||||
51 QGTAALQKELKRIKIPDYSDFEIKHLKGCHYFYSMDIREFQLPSSQIS 100
  |||||
1101 MVPNVGLKFESISNANIKISGKWKAQKRFKMGSGNFDLSIEGMSISADLKL 150
  |||||
1101 MVPNVGLKFESISNANIKISGKWKAQKRFKMGSGNFDLSIEGMSISADLKL 150
  |||||
1151 GSNPTSGKPTTTCSSCSSHINSVHVHISKSKVGWLIQLFHKKIESALRNK 200
  |||||
1151 GSNPTSGKPTTTCSSCSSHINSVHVHISKSKVGWLIQLFHKKIESALRNK 200
  |||||
201 MNSQVCEKVTNSVSSKLQPYFQTLPVMTKIDSVAGINYGLVAPPATTAET 250
  |||||
201 MNSQVCEKVTNSVSSKLQPYFQTLPVMTKIDSVAGINYGLVAPPATTAET 250
  |||||

```

Fig. 1

251 LDVQMKGEFYSENHHNPPPPFAPPVMEFFPAAHDRMVYLGSLDYFFENTAGLV 300  
|||||  
251 LDVQMKGEFYSENHHNPPPPFAPPVMEFFPAAHDRMVYLGSLDYFFENTAGLV 300  
|||||  
301 YQEAGVLKMTLRDDMIPKESKERLTTKFFGTFLPEVAKKFPNMKIQIHVS 350  
|||||  
301 YQEAGVLKMTLRDDMIPKESKERLTTKFFGTFLPEVAKKFPNMKIQIHVS 350  
|||||  
351 ASTPPHLSVQPTGLTFYPADVQAFVLPNSSLASLFLIGM 391  
|||||  
351 ASTPPHLSVQPTGLTFYPADVQAFVLPNSSLASLFLIGM 391

Fig. 1 (Cont.)

2

251 KNPLFWAKKVAEKVGCPCVGDAARMAQCLKVTDPRALTLAYKVPLAGLEYP 300  
|||||  
251 KNPLFWAKKVAEKVGCPCVGDAARMAQCLKVTDPRALTLAYKVPLAGLEYP 300  
  
301 MLHYVGFVPVIDGDFIPADPINLYANAADIDYIAGTNNMDGHIFASIDMP 350  
|||||  
301 MLHYVGFVPVIDGDFIPADPINLYANAADIDYIAGTNNMDGHIFASIDMP 350  
  
351 AINKGNKKVTEEDFYKLVSEFTITKGLRGAKTTFDVYTESWAQDPSQENK 400  
|||||  
351 AINKGNKKVTEEDFYKLVSEFTITKGLRGAKTTFDVYTESWAQDPSQENK 400  
  
401 KKTVVDFEETDVLFLVPTETIALAQHRANAKSAKTYAYLFESHPSRMPVYPKW 450  
|||||  
401 KKTVVDFEETDVLFLVPTETIALAQHRANAKSAKTYAYLFESHPSRMPVYPKW 450  
  
451 VGADHADDIQYVFGKPFATPTGYRPODRTVSKAMIAYTWNFAKTGDPNMG 500  
|||||  
451 VGADHADDIQYVFGKPFATPTGYRPODRTVSKAMIAYTWNFAKTGDPNMG 500

Fig. 2 (Cont.)

501 DSAVPTHWEPTYTENS GYLEITKKMGSSSMKRSLRTNFLRYWTLTYLALP 550  
|||||  
501 DSAVPTHWEPTYTENS GYLEITKKMGSSSMKRSLRTNFLRYWTLTYLALP 550  
551 TVTDQEATVPVPTG DSEATVPVPTG DSETAPVPTG DSGAPPVPTG DSG 600  
|||||  
551 TVTDQEATVPVPTG DSEATVPVPTG DSETAPVPTG DSGAPPVPTG DSG 600  
601 APPVPTG DSGAPPVPTG DSEA 623  
|||||  
601 APPVPTG DSGAPPVPTG DSGA 623

Fig. 2 (Cont.)

Fig. 3

Fig. 3

251 QARNWGLGGHAFRCRNPNDNDIRPWCFLNDRDRLSWEYCDLAQCQTPTQAAP 300  
|||||  
254 QARNWGLGGHAFRCRNPNDNDIRPWCFLNDRDRLSWEYCDLAQCQTPTQAAP 303  
|||||  
301 PTPVSPRLHVPLMPAQAPPKPQPTTRTPPQSQTTPGALPAKREQPPSLTR 353  
|||||  
304 PTPVSPRLHVPLMPAQAPPKPQPTTRTPPQSQTTPGALPAKREQPPSLTR 353  
|||||  
351 NGPLSCGQRLRKSLSSMTRVVGGLVALRGAHPYIAALYWGHSHFCAGSLIA 403  
|||||  
354 NGPLSCGQRLRKSLSSMTRVVGGLVALRGAHPYIAALYWGHSHFCAGSLIA 403  
|||||  
401 PCWVLTAAHCLQDRPAPEDLTVVLGQERRNHSCEPCQTLAVRSYRLHEAF 453  
|||||  
404 PCWVLTAAHCLQDRPAPEDLTVVLGQERRNHSCEPCQTLAVRSYRLHEAF 453  
|||||  
451 SPVSYQHDLALLRLQEDADGSCALLSPYVQPVCLPSGAARPSETTLCQVA 503  
|||||  
454 SPVSYQHDLALLRLQEDADGSCALLSPYVQPVCLPSGAARPSETTLCQVA 503  
|||||

Fig. 3 (Cont.)

501 GWGHQFEAEYASFLQEAQVPFLSLERCSAPDVHGSSILPGMLCAGFLE 550  
 |||||  
 504 GWGHQFEAEYASFLQEAQVPFLSLERCSAPDVHGSSILPGMLCAGFLE 553  
 |||||  
 551 GGTDACAGELLAGWRPSRPSAXSQVHSADCVFPTQDSDGGPLVCEQAA 600  
 |||||  
 554 GGTDAC.....QGDSGGPLVCEQAA 574  
 601 ERRLTQGIISWGSGCCDRNKPVGYYTDVAYYLAWIREHTVS 641  
 |||||  
 575 ERRLTQGIISWGSGCCDRNKPVGYYTDVAYYLAWIREHTVS 615

Fig. 3 (Cont.)



**Fig. 4**

1 MAPFEPLASGILLLLWLIAPSRACCTCVPPHPQTAFNCSDLVIRAKFVGTP 50  
 1 MAPFEPLASGILLLLWLIAPSRACCTCVPPHPQTAFNCSDLVIRAKFVGTP 50  
 51 EVNQTTLYQRYEIKMTKMYKGFGQALGDAADIRFVYTPAMESVCGYFHRSH 100  
 51 EVNQTTLYQRYEIKMTKMYKGFGQALGDAADIRFVYTPAMESVCGYFHRSH 100  
 101 NRSEEFLLIAGKLQ 113  
 101 NRSEEFLLIAGKLQ 113

**Fig. 5**

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1 MAPFEPLASGILLLLWLIAPSRACCTCVPPHPQTAFCNSDLVIRAKFVGTP 50  
|||||  
1 MAPFEPLASGILLLLWLIAPSRACCTCVPPHPQTAFCNSDLVIRAKFVGTP 50  
51 EVNQTTLYQRYEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSH 100  
|||||  
51 EVNQTTLYQRYEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSH 100  
101 NRSEEFLLI..... 108  
|||||  
101 NRSEEFLLIAGKLQDGLLHITTCSFVAPWNLSLAQRGRFTKTYTVGCEEC 150  
109 .....LSIPCKLQSGTHCLWTDQLLQSEKGFQSRHLACLPREPGLCTWQ 153  
|||||  
151 TVFPCLIPCKLQSGTHCLWTDQLLQSEKGFQSRHLACLPREPGLCTWQ 200  
154 SLRSQIA 160  
|||||  
201 SLRSQIA 207

Fig. 7

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Fin.

6. **Fi**

251 ENQWFAAIYRRHGGSVTVVCGGSLISPCWVISATHCFIDYPKKEDYIV 300  
 |||||  
 188 ENQWFAAIYRRHGGSVTVVCGGSLISPCWVISATHCFIDYPKKEDYIV 237  
 |||||  
 301 YLGRSRLNSNTQGMKFEVENLILHKDYSADTLAHNDIALLKIRSKEGR 287  
 |||||  
 238 YLGRSRLNSNTQGMKFEVENLILHKDYSADTLAHNDIALLKIRSKEGR 400  
 |||||  
 351 CAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMTVV 337  
 |||||  
 288 CAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMTVV 450  
 |||||  
 401 KLISHRECQPHYGGSEVTKMLCAADPQWKTDSCQGDGGPLVCSLQCR 387  
 |||||  
 338 KLISHRECQPHYGGSEVTKMLCAADPQWKTDSCQGDGGPLVCSLQCR 494  
 |||||  
 451 MTLTGIVSWGRCALKDKPGVYTRVSHFLPWIRSHTEENGLAL 431  
 |||||  
 388 MTLTGIVSWGRCALKDKPGVYTRVSHFLPWIRSHTEENGLAL

Fig. 9 (Cont.)

1 MQMSPALTCLVLGLALVFEGESAVHHPPSYVAHLASDFGVRVFQQVAQAS 50  
|||||  
1 MQMSPALTCLVLGLALVFEGESAVHHPPSYVAHLASDFGVRVFQQVAQAS 50  
51 KDRNVVFSPYGVASVLAMLQLTTGGETQQQIQAAAMGFKIDDKGMAPALRH 100  
|||||  
51 KDRNVVFSPYGVASVLAMLQLTTGGETQQQIQAAAMGFKIDDKGMAPALRH 100  
101 LYKELMGPWNKDEISTDAIFVQORDLKLVOGFMPHFRLFRSTVVKQVDFS 150  
|||||  
101 LYKELMGPWNKDEISTDAIFVQORDLKLVOGFMPHFRLFRSTVVKQVDFS 150  
151 EVERARFIINDWVKTHTKGMISNLLGKGAVDQLTRLVLVNALYFNGQWKT 200  
|||||  
151 EVERARFIINDWVKTHTKGMISNLLGKGAVDQLTRLVLVNALYFNGQWKT 200  
201 PFPDSSTHRRLEFHKS DGS TVSVPMMAQTNKFNYTEFTTPDGHYYDILELP 250  
|||||  
201 PFPDSSTHRRLEFHKS DGS TVSVPMMAQTNKFNYTEFTTPDGHYYDILELP 250  
251 YHGD T L S M F I A A D L . . . V P T E A L 270  
|||||  
251 YHGD T L S M F I A A P Y E K E V P L S A L 273

Fig. 10



**Fig. 11**

**Fig. 11 (Cont.)**

**Fig. 12**

**Fig. 12**

169 VQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLCMVRPCEADLEENI 218  
|||||  
201 VQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLCMVRPCEADLEENI 250  
|||||  
219 KKGKKCIRTPKISKPIKFEELSGCTSMKTYRAKFCGVCTDGRCCTPHRTTT 268  
|||||  
251 KKGKKCIRTPKISKPIKFEELSGCTSMKTYRAKFCGVCTDGRCCTPHRTTT 300  
|||||  
269 LPVEEFKCPDGEVNMKKNMMFIKTCACHYNCPGDNDIFESLYRKMYGDMA 317  
|||||  
301 LPVEEFKCPDGEVNMKKNMMFIKTCACHYNCPGDNDIFESLYRKMYGDMA 349  
|||||

Fig. 12 (Cont.)

**Fig. 13**

253 AIEGKDAVLECCVSGYPPPSFTWLRGEEVIQLRSKKYSLGGSNLLISNV 302  
|||||  
251 AIEGKDAVLECCVSGYPPPSFTWLRGEEVIQLRSKKYSLGGSNLLISNV 300  
303 TDDDSGMYTCVVVTYKNENISASAELTVLV 331  
|||||  
301 TDDDSGMYTCVVVTYKNENISASAELTVLV 329

Fig. 13 (Cont.)

3 MENSIRCVWVPKLAFLVLFASLLSAHLQVTGFQIKAFALRFLSEPSDAV 52  
|||||  
1 MENSIRCVWVPKLAFLVLFASLLSAHLQVTGFQIKAFALRFLSEPSDAV 50  
53 TMRGGNVLLDCSAESDRGVPVIKWKDAIHLALGMDERKQQLSNGSLLIQ 102  
|||||  
51 TMRGGNVLLDCSAESDRGVPVIKWKDGIHLALGMDERKQQLSNGSLLIQ 100  
103 NILHSRHHKPDDEGLYQCEASLGDSGSIISRTAKVAVAGPLRFLSQTESVT 152  
|||||  
101 NILHSRHHKPDDEGLYQCEASLGDSGSIISRTAKVAVAGPLRFLSQTESVT 150  
153 AFMGDTVLLKCEVIGEPMTIHWQKNQODLTPIPGDSRVVVLPSGALQIS 202  
|||||  
151 AFMGDTVLLKCEVIGEPMTIHWQKNQODLTPIPGDSRVVVLPSGALQIS 200  
203 RLQPGDIGIYRCSARNPASSRTGNEAEVRILSDPGLHRQLYFLQRPNSVV 252  
|||||  
201 RLQPGDIGIYRCSARNPASSRTGNEAEVRILSDPGLHRQLYFLQRPNSVV 250  
253 AIEGKDAVLECCVSGYPPPSFTWLRGEEVIQLRSKKYSLLGGSNLLISNV 302  
|||||  
251 AIEGKDAVLECCVSGYPPPSFTWLRGEEVIQLRSKKYSLLGGSNLLISNV 300

Fig. 14

**Fig. 14 (Cont.)**



603	YNRYGPGVSTDDITVVTLS	DVPSAPPQNV	SLFVVNSRSIKVSWLPPPSGT	652
601	YNRYGPGVSTDDITVVTLS	DVPSAPPQNV	SLFVVNSRSIKVSWLPPPSGT	650
653	QNGFITGYKIRHRKTTRRG	EMETLEPNNLWYLETGLEKGSQ	YSFQVSAMT	702
651	QNGFITGYKIRHRKTTRRG	EMETLEPNNLWYLETGLEKGSQ	YSFQVSAMT	700
703	VNGTGPPSNWYTAETPENDL	DESQVPDQPSSLHVRPQTNCI	IMSWTPPLN	752
701	VNGTGPPSNWYTAETPENDL	DESQVPDQPSSLHVRPQTNCI	IMSWTPPLN	750
753	PNIVVRGYIIGYGVGSPYA	ETVRVDSKQRYYSIERLESSH	YVISLKAEN	802
751	PNIVVRGYIIGYGVGSPYA	ETVRVDSKQRYYSIERLESSH	YVISLKAEN	800
803	NAGECVPLYESATTRSITD	PTDPVDYYPLLDDFPTSVPDL	STPMLPPGV	852
801	NAGECVPLYESATTRSITD	PTDPVDYYPLLDDFPTSVPDL	STPMLPPGV	850
853	QAVALTHDAVRVSWADNS	VPKNQKTSEVRLYTVRWRTS	FSASAKYKSED	902
851	QAVALTHDAVRVSWADNS	VPKNQKTSEVRLYTVRWRTS	FSASAKYKSED	900

**Fig. 14 (Cont.)**

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**Fig. 14 (Cont.)**

1203 KSTSHSGQDTEEAGSSMSTLERSLAARRAPRAKLMIPMDAQNNPAVVSA 1252  
|||||  
1201 KSTSHSGQDTEEAGSSMSTLERSLAARRAPRAKLMIPMDAQNNPAVVSA 1250  
|||||  
1253 IPVPTLESAQYPGILPSPTCGYPHPQFTLRPVPEFTLSVDRGEFAGRSQS 1302  
|||||  
1251 IPVPTLESAQYPGILPSPTCGYPHPQFTLRPVPEFTLSVDRGEFAGRSQS 1300  
|||||  
1303 VSEGPTTQQPPMLPPSQPEHSSSEEEAPSRPTIACVRPTHPLRSFANPLL 1352  
|||||  
1301 VSEGPTTQQPPMLPPSQPEHSSSEEEAPSRPTIACVRPTHPLRSFANPLL 1350  
|||||  
1353 PPPMSAIEPKVPYTPLLSQPGPTLPKTHVKTASLGLAGKARSPLLPVSV 1402  
|||||  
1351 PPPMSAIEPKVPYTPLLSQPGPTLPKTHVKTASLGLAGKARSPLLPVSV 1400  
|||||  
1403 TAPEVSEESHKPTEDSANV 1421  
|||||  
1401 TAPEVSEESHKPTEDSANV 1419

Fig. 14 (Cont.)

1 MPGKRGWGWWARLPLCLLLSLYGPWMPSSLGKPKGHPHMNSIRIDGIT 50  
|||||  
1 MPGKRGWGWWARLPLCLLLSLYGPWMPSSLGKPKGHPHMNSIRIDGIT 50  
  
51 LGGLEFPVHGRGSEKPCGELKKKEKGIHRLLEAMLFALDRINNDPDLNPIT 100  
|||||  
51 LGGLEFPVHGRGSEKPCGELKKKEKGIHRLLEAMLFALDRINNDPDLNPIT 100  
  
101 LGARILDTCSRDTHALEQSLTFVQALIEKDGTEVRCGSGGPPITTKPERV 150  
|||||  
101 LGARILDTCSRDTHALEQSLTFVQALIEKDGTEVRCGSGGPPITTKPERV 150  
  
151 VGVIGASGSSVSIMVANIILRFKIPQISYASTAPDLSNDRYDFFSRVVP 200  
|||||  
151 VGVIGASGSSVSIMVANIILRFKIPQISYASTAPDLSNDRYDFFSRVVP 200  
  
201 SDTYQAQAMVDIVRAIKWNVSTVASEGSYGESGVEAFIQKSREDGGVCI 250  
|||||  
201 SDTYQAQAMVDIVRAIKWNVSTVASEGSYGESGVEAFIQKSREDGGVCI 250  
  
251 AQS VKIPREP KAGEFDKIIRRLLETSNARAVIIFANEDDIRRVLEAARRA 300  
|||||  
251 AQS VKIPREP KAGEFDKIIRRLLETSNARAVIIFANEDDIRRVLEAARRA 300

Fig. 15

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301 NQTGHFFWMSGDSWGSKIAPVLHLEEVAEGAVTILPKRMSVR..... 342
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
301 NQTGHFFWMSGDSWGSKIAPVLHLEEVAEGAVTILPKRMSVRGFDRYESS 350

343 .....DRERIGQDSAY 353
    . | | | | | | | | | | | | | | | | | | | | | | | | | | | |
351 RTLDNNRRNIWFEEFWEDNEFHCKLSRHALKKGSHVKKCTNRERIGQDSAY 400

354 EQEGKVQFVIDAVYAMGHALHAMHRDLCPRVGLCPRMDPVDGTQLLKYI 403
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
401 EQEGKVQFVIDAVYAMGHALHAMHRDLCPRVGLCPRMDPVDGTQLLKYI 450

404 RNVNFSGIAGNPVTFNENGDAPEGRIYQYQLRNDSEYKVIGSWTDHLH 453
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
451 RNVNFSGIAGNPVTFNENGDAPEGRIYQYQLRNDSEYKVIGSWTDHLH 500

454 LRIERMHWPGSGQQLPRSLPCQPGERKKTVKGMPCCHCEPCTGYQY 503
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
501 LRIERMHWPGSGQQLPRSLPCQPGERKKTVKGMPCCHCEPCTGYQY 550

504 QVDRYTCKTCPYDMRPTENRTGCRPIPIKLEWGSPWAVLPLFLAVVGIA 553
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
551 QVDRYTCKTCPYDMRPTENRTGCRPIPIKLEWGSPWAVLPLFLAVVGIA 600

```

Fig. 15 (Cont.)

554 ATLEFVITFVRYNDTPIVKASGRELSYVLLAGIFLCYATTFMLIAEPDLG 603  
|||||  
601 ATLEFVITFVRYNDTPIVKASGRELSYVLLAGIFLCYATTFMLIAEPDLG 650  
  
604 TCSLRRIFLGLGMSISYAALLTKTNRIYRIFEQGRSVSAPRFISPASQL 653  
|||||  
651 TCSLRRIFLGLGMSISYAALLTKTNRIYRIFEQGRSVSAPRFISPASQL 700  
  
654 AITFSLISLQLLGICVWFVVDPSHSVDFQDQRTLDPRFARGVLKCDISD 703  
|||||  
701 AITFSLISLQLLGICVWFVVDPSHSVDFQDQRTLDPRFARGVLKCDISD 750  
  
704 LSLICLLGYSMLLMVTCTVYAIKTRGVPETENEAKPIGFTMYTTCIVWLA 753  
|||||  
751 LSLICLLGYSMLLMVTCTVYAIKTRGVPETENEAKPIGFTMYTTCIVWLA 800

Fig. 15 (Cont.)

754 FIPIFFGTSQSADKLYIQTTTLTVSVLSASVSLGMLYMPKVYIILFHPE 803  
|||||  
801 FIPIFFGTSQSADKLYIQTTTLTVSVLSASVSLGMLYMPKVYIILFHPE 850  
  
804 QNVPKRKRSLKAVVTAATMSNKFTQKGNFRPNGEAKSELCEALEAPALAT 853  
|||||  
851 QNVPKRKRSLKAVVTAATMSNKFTQKGNFRPNGEAKSELCEALEAPALAT 900

854 KQTYVTTYTNHAI 865  
|||||  
901 KQTYVTTYTNHAI 912

Fig. 15 (Cont.)

**Fig. 16**



301 ANINNSRCSVSSPSNTNRRSTLSSPAASTVGSICSPVNNAFSYTASG TSA 350  
|||||  
301 ANINNSRCSVSSPSNTNRRSTLSSPAASTVGSICSPVNNAFSYTASG TSA 350  
351 GSSTLRDVVPSPDTQEKGAQEVFPFKTEEVESAISNGVTGQLNIVQYIKP 400  
|||||  
351 GSSTLRDVVPSPDTQEKGAQEVFPFKTEEVESAISNGVTGQLNIVQYIKP 400  
401 EPDGAFFSSCLGGNSKINSDSSFSVPKQESTKHSCSGTSFKGNPTVNP 450  
|||||  
401 EPDGAFFSSCLGGNSKINSDSSFSVPKQESTKHSCSGTSFKGNPTVNP 450  
451 PFMDGSYFSEFMDDKDYSLGILPPVPFGDGNCEGSGFPVGIKQEPDDG 500  
|||||  
451 PFMDGSYFSEFMDDKDYSLGILPPVPFGDGNCEGSGFPVGIKQEPDDG 500  
501 SYYPEASIPSSAIVGVNSGGQSFHYRIGAQGTISLSRSARDQSFQHLSSF 550  
|||||  
501 SYYPEASIPSSAIVGVNSGGQSFHYRIGAQGTISLSRSARDQSFQHLSSF 550  
551 PPVNTLVESWKSHGDLSSRRSDGYPVLEYIPENVSSSTLRSVSTGSSRPS 600  
|||||  
551 PPVNTLVESWKSHGDLSSRRSDGYPVLEYIPENVSSSTLRSVSTGSSRPS 600

Fig. 16 (Cont.)

**Fig. 16 (Cont.)**

Fig. 17

Fig. 17

301 ANINNSRCVSSPSNTNRRSTLSSPAASTVGSICSPVNNAFSYTAGTSA 350  
|||||  
301 ANINNSRCVSSPSNTNRRSTLSSPAASTVGSICSPVNNAFSYTAGTSA 350  
351 GSSTLRDVVPSPDTQEKGAQEVPPKTEEVESAISNGVTGQLNIVQYIKP 400  
|||||  
351 GSSTLRDVVPSPDTQEKGAQEVPPKTEEVESAISNGVTGQLNIVQYIKP 400  
401 EPDGAFFSSCLGNSKINSDDSSFSVPIKQESTKHSCSGTSFKGNPTVNP 450  
|||||  
401 EPDGAFFSSCLGNSKINSDDSSFSVPIKQESTKHSCSGTSFKGNPTVNP 450  
451 PFMDGSYFSEFMDKDYYSLSGILPPVPGFDGNCESGFPVGIKQEPDDG 500  
|||||  
451 PFMDGSYFSEFMDKDYYSLSGILPPVPGFDGNCESGFPVGIKQEPDDG 500  
501 SYYPEASIPSSAIVGVNSGGQSFHYRIGAQGTISLSRSARDQSFQHLSSF 550  
|||||  
501 SYYPEASIPSSAIVGVNSGGQSFHYRIGAQGTISLSRSARDQSFQHLSSF 550  
551 PPVNTLVESWKSHGDLSSRRSDGYPVLEYIPENVSSSLRSVSTGSSRPS 600  
|||||  
551 PPVNTLVESWKSHGDLSSRRSDGYPVLEYIPENVSSSLRSVSTGSSRPS 600

Fig. 17 (Cont.)

601 KICLVCGDEASGCHYGVVTCGSCCKVEFFKRAVEGQHNYLCAGRNDCIIDKI 650  
|||||  
601 KICLVCGDEASGCHYGVVTCGSCCKVEFFKRAVEGQHNYLCAGRNDCIIDKI 650

651 RRKNCPACRLQKCLQAGMNLGARKSKKLGLKGIIHEEQPQQQP PPPPP 700  
|||||  
651 RRKNCPACRLQKCLQAGMNLGARKSKKLGLKGIIHEEQPQQQP PPPPP 700

701 PQSPEEGTTYIAPAKEPSVNTALVPQLSTISRALTSPVMVLENIEPEIV 750  
|||||  
701 PQSPEEGTTYIAPAKEPSVNTALVPQLSTISRALTSPVMVLENIEPEIV 750

751 YAGYDSSKPDPDTAENLLSTLNRLAGKOMIQVVKWAKVLPGFKNLPLEDQIT 800  
|||||  
751 YAGYDSSKPDPDTAENLLSTLNRLAGKOMIQVVKWAKVLPGFKNLPLEDQIT 800

801 LIQYSWMCLISSEFALSWSRSYKHHTNSOFLYFAPDLVFNE 837  
|||||  
801 LIQYSWMCLISSEFALSWSRSYKHHTNSOFLYFAPDLVFNE 837

**Fig. 17 (Cont.)**

1 MGRQLVVLGLTCCWAVASAAKLGAVYTEGGFVEGVNKKLGLLGDSDVDF 50  
|||||  
1 MGRQLVVLGLTCCWAVASAAKLGAVYTEGGFVEGVNKKLGLLGDSDVDF 50  
51 KGIPFAAPT KALENPQPHPGWQGT LKAKNFKKRC LQATITQDSTYGDEDC 100  
|||||  
51 KGIPFAAPT KALENPQPHPGWQGT LKAKNFKKRC LQATITQDSTYGDEDC 100  
101 LYLNIWVPQGRKQVSRDLPVMIWIYGAFLMGSGHGANFLNNLYDGE EI 150  
|||||  
101 LYLNIWVPQGRKQVSRDLPVMIWIYGAFLMGSGHGANFLNNLYDGE EI 150  
151 ATRGNVIVVTENYRVGPLGFLSTGDANLPGNYGLRDQHMAIAWVKRNIAA 200  
|||||  
151 ATRGNVIVVTENYRVGPLGFLSTGDANLPGNYGLRDQHMAIAWVKRNIAA 200  
201 FGGDPNNITLFGESAGGASVSLQTLSPYNKGLIRRAISQSGVALSPWVIQ 250  
|||||  
201 FGGDPNNITLFGESAGGASVSLQTLSPYNKGLIRRAISQSGVALSPWVIQ 250

Fig. 18

251 KNPLFWAKKVAEKVCGPVGDAARMAQCLKVTDPRALTLAYKVPLAGLEYP 300  
 |||||  
 251 KNPLFWAKKVAEKVCGPVGDAARMAQCLKVTDPRALTLAYKVPLAGLEYP 300  
 |||||  
 301 MLHYVGFVPVIDGDFIPADPINLYANAADIDYIAGTNNMDGHIFASIDMP 350  
 |||||  
 301 MLHYVGFVPVIDGDFIPADPINLYANAADIDYIAGTNNMDGHIFASIDMP 350  
 |||||  
 351 AINKGNKKVTEEDFYKLVSEFTITKGLRGAKTTFDVYTESWAQDPSQENK 400  
 |||||  
 351 AINKGNKKVTEEDFYKLVSEFTITKGLRGAKTTFDVYTESWAQDPSQENK 400  
 |||||  
 401 KKTVDFFETDVLFLVPTEIALAQHRANAKSAKTYAYLFESHPSRMPVYPKW 450  
 |||||  
 401 KKTVDFFETDVLFLVPTEIALAQHRANAKSAKTYAYLFESHPSRMPVYPKW 450  
 |||||  
 451 VGADHADDIQYVFGKPEFATPTGYRPQDRTVSKAMIAYWNTNFAKTGDPNMG 500  
 |||||  
 451 VGADHADDIQYVFGKPEFATPTGYRPQDRTVSKAMIAYWNTNFAKTGDPNMG 500  
 |||||

Fig. 18 (Cont.<sup>1</sup>)

501 DSAVPTHWEPTYTENS GYLEITKKMGSSMKRSLRTNFLRYWTLTYLALP 550  
|||||  
501 DSAVPTHWEPTYTENS GYLEITKKMGSSMKRSLRTNFLRYWTLTYLALP 550  
551 TVTDQEATPVPPPTG DSEATPVPPPTG DSEATAPVPPPTG DSGAPPVPPTG DSG 600  
|||||  
551 TVTDQEATPVPPPTG DSEATPVPPPTG DSEATAPVPPPTG DSGAPPVPPTG DSG 600  
601 APPVPPTG DSGAPPVPPTG DSGAPPVPPTG DSGAPPVP 639  
|||||  
601 APPVPPTG DSGAPPVPPTG DSGAPPVPPTG DSGAPPVP 639

Fig. 18 (Cont.<sup>2</sup>)



**Fig. 19**

1 MKTYRAKFCGVCTDGRCCCTPHRTTTLPEFKCPDGEVMKKNNMMFIKTCAC 50  
|||||  
276 MKTYRAKFCGVCTDGRCCCTPHRTTTLPEFKCPDGEVMKKNNMMFIKTCAC 325

51 HYNCPGDNDIFESLYYRKMYGDMA 74  
|||||  
326 HYNCPGDNDIFESLYYRKMYGDMA 349

Fig. 20

1 MTAASMGPVVRAFVLLALCSRPAVGQNCSGPCRCDEPAPRCPAGVSLV 50  
|||||  
1 MTAASMGPVVRAFVLLALCSRPAVGQNCSGPCRCDEPAPRCPAGVSLV 50  
51 LDGCGCCRVCAKQLGELCTERDPCDPHKGLECFDGFSPANRKIGVCTAKDG 100  
|||||  
51 LDGCGCCRVCAKQLGELCTERDPCDPHKGLECFDGFSPANRKIGVCTAKDG 100  
101 APCIFGGTVYRSGESFQSSCKYQCTCLDGAVGCMPLCSMDVRLPSPDCPF 150  
|||||  
101 APCIFGGTVYRSGESFQSSCKYQCTCLDGAVGCMPLCSMDVRLPSPDCPF 150  
151 P 151  
151 P 151

Fig. 21

**Fig. 22**

```

1 MAPFEPLASGILLLLWLIAPSRACVCVPPHPQTAFNCNSDLVIRAKFVGTP 50
  |||||
1 MAPFEPLASGILLLLWLIAPSRACVCVPPHPQTAFNCNSDLVIRAKFVGTP 50

51 EVNQTTLYQRYEIKMTKMYKGFQALXDAADIRFVYTPAMESVCCGYFHRSH 100
  |||||
51 EVNQTTLYQRYEIKMTKMYKGFQALGDAADIRFVYTPAMESVCCGYFHRSH 100

101 NRS 103
  |||
101 NRS 103

```

Fig. 23



**Fig. 25**

1 MTKMYKGEQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLLIAGKLQD 50  
|||||  
65 MTKMYKGEQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLLIAGKLQD 114  
51 GLLHITTCFVAPWNLSLAQRRGFTKTYTVGCCECTVFPCLSI PCKLQS 100  
|||||  
115 GLLHITTCFVAPWNLSLAQRRGFTKTYTVGCCECTVFPCLSI PCKLQS 164  
101 GTHCLWTDQLLQSEKGFQSRHLACLPREPGLCTWQSLRSQIA 143  
|||||  
165 GTHCLWTDQLLQSEKGFQSRHLACLPREPGLCTWQSLRSQIA 207

Fig. 26